

FIG. 1

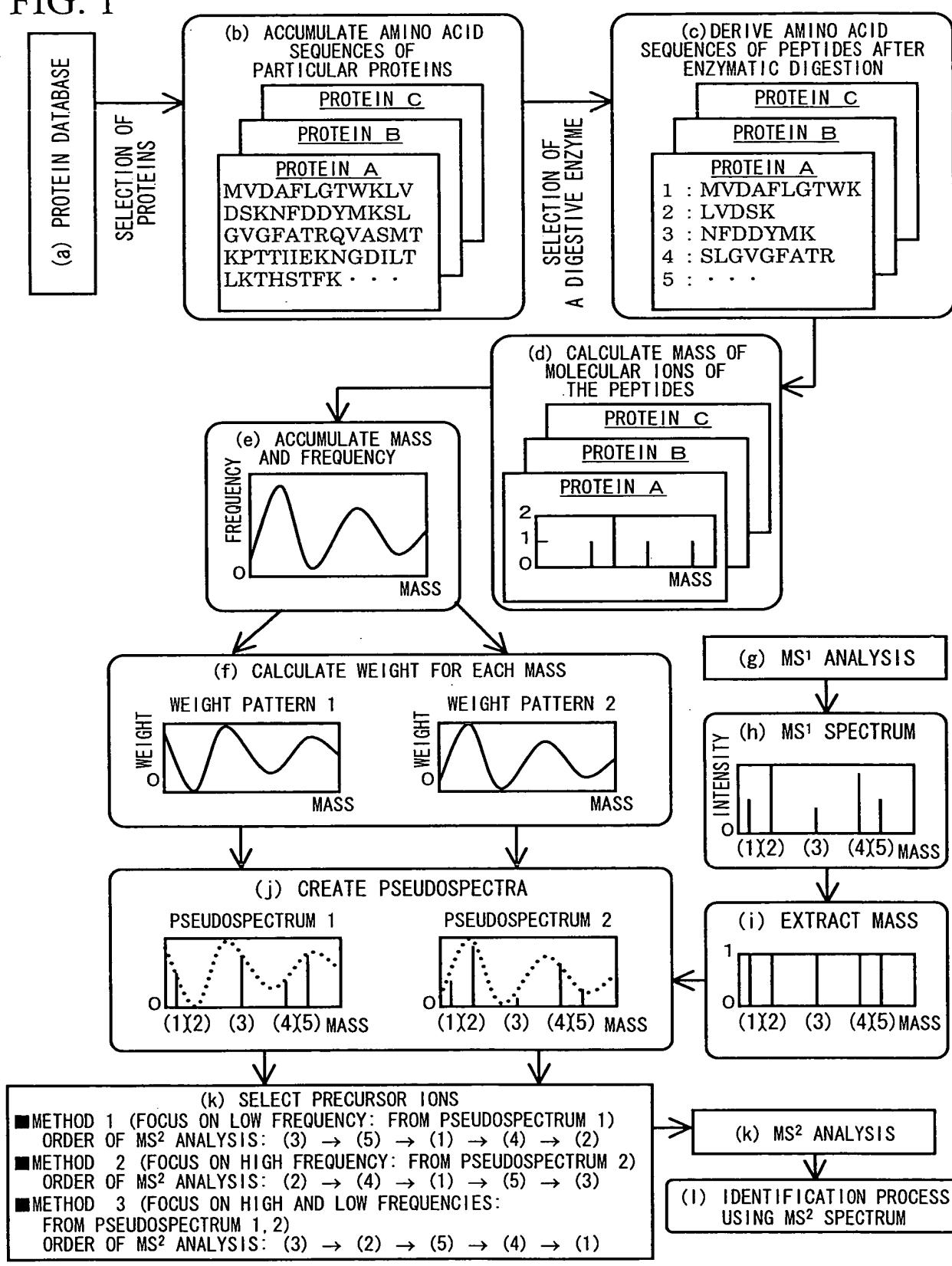


FIG. 2

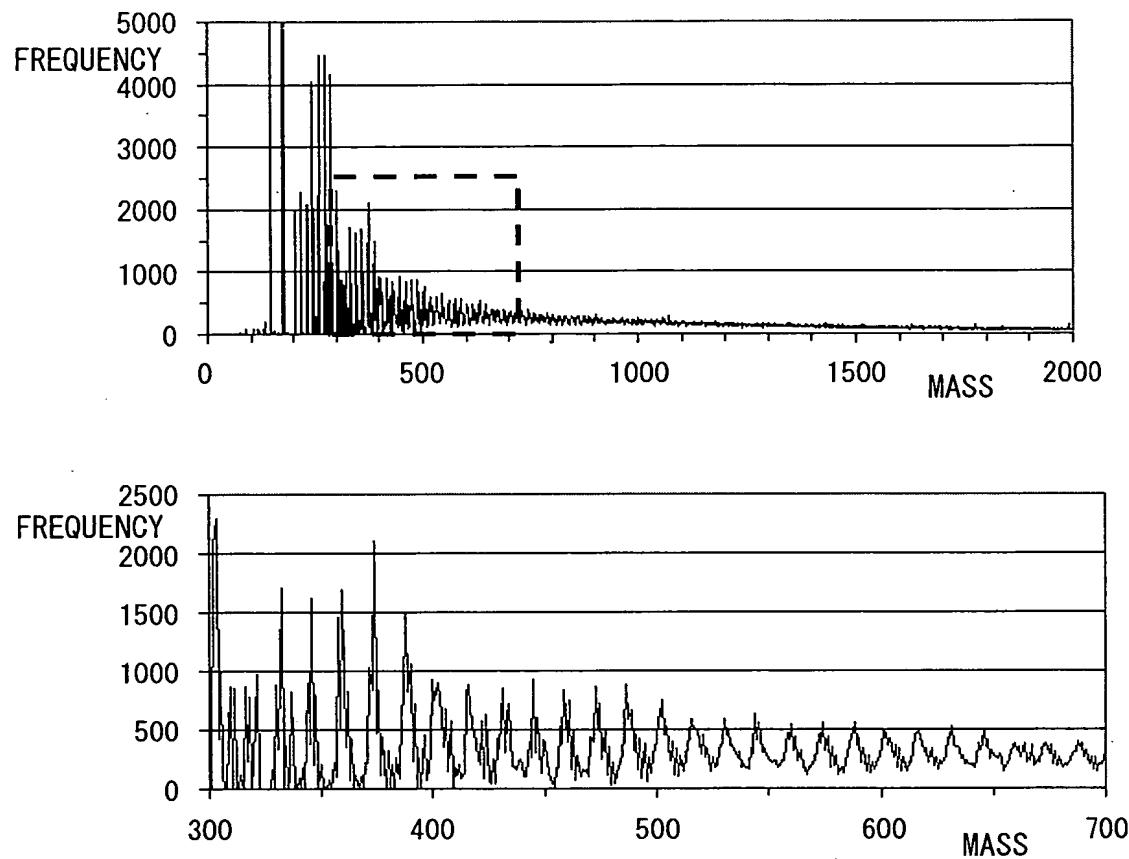


FIG. 3

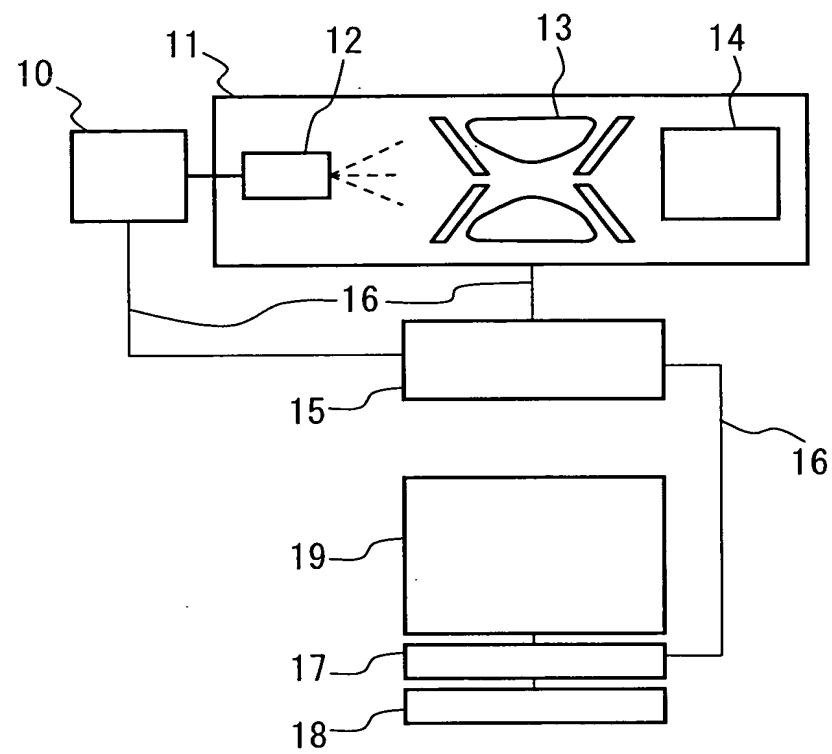


FIG. 4

(a) PROTEIN SELECTION CONDITIONS

DATABASE	Swiss-prot	SPECIES	homo sapiens
KEYWORD	zinc finger		

(b) FREQUENCY AND WEIGHT PATTERN CALCULATION CONDITIONS

MODIFICATION	<input type="checkbox"/> PHOSPHORIZATION	<input type="checkbox"/> ACETYLATION	<input type="checkbox"/> METHYLATION
DIGESTIVE ENZYME	Trypsin		
METHOD OF IONIZATION	ESI		
MASS ACCURACY (Da)	1		
MASS RANGE (Da)	50	—	40000
MASS TYPE	<input checked="" type="radio"/> MONOISOTOPIC <input type="radio"/> AVERAGE		

(c) FREQUENCY AND WEIGHT PATTERN CALCULATION RESULTS

FREQUENCY
  WEIGHT PATTERN 1
  WEIGHT PATTERN 2

(d) PRECURSOR ION SELECTION AND MS/MS ANALYSIS CONDITIONS

MASS RANGE (Da)	300	—	40000
THRESHOLD OF ION INTENSITY	10	%	<input type="checkbox"/>
PSEUDOSPECTRUM INTENSITY (LOW FREQUENCY)	0. 5	—	0. 001
PSEUDOSPECTRUM INTENSITY (HIGH FREQUENCY)	1	—	0. 01
PRECURSOR ION	<input checked="" type="radio"/> FROM LOW FREQUENCY <input type="radio"/> FROM HIGH FREQUENCY <input checked="" type="radio"/> HIGH → LOW ALTERNATELY <input type="radio"/> LOW → HIGH ALTERNATELY		
MS/MS ANALYSIS REPETITION	3	TIMES	<input type="checkbox"/>

FIG. 5

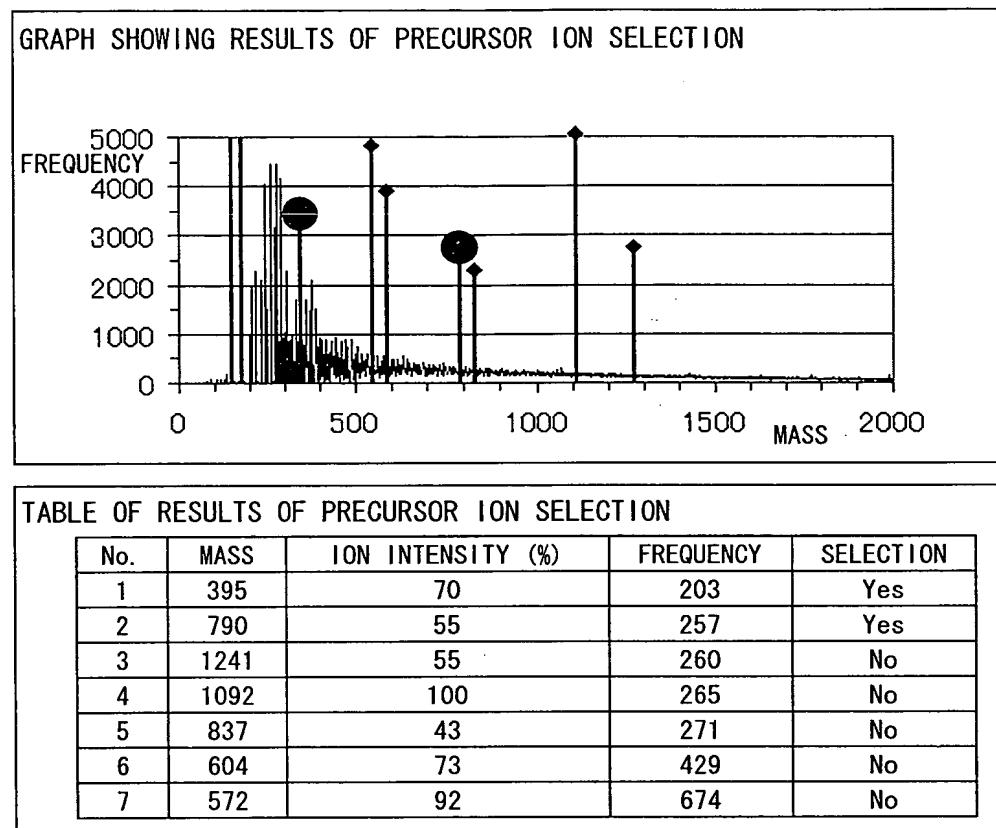


FIG. 6

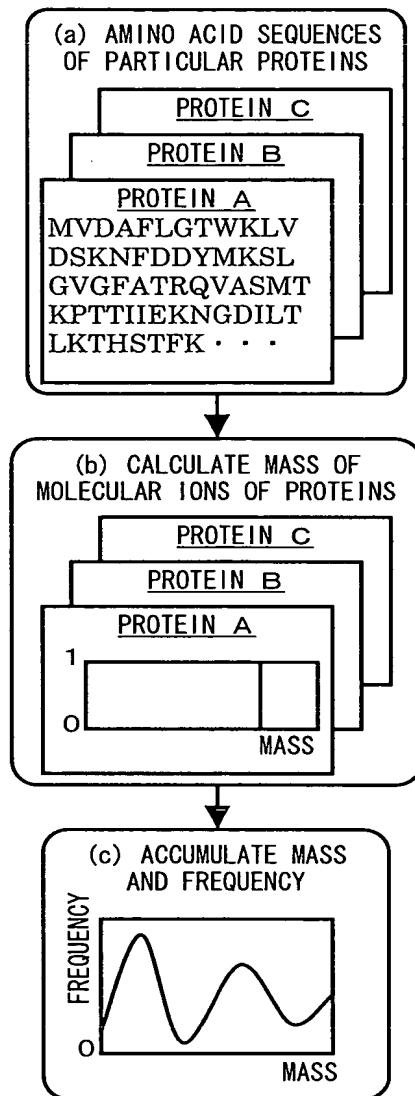


FIG. 7

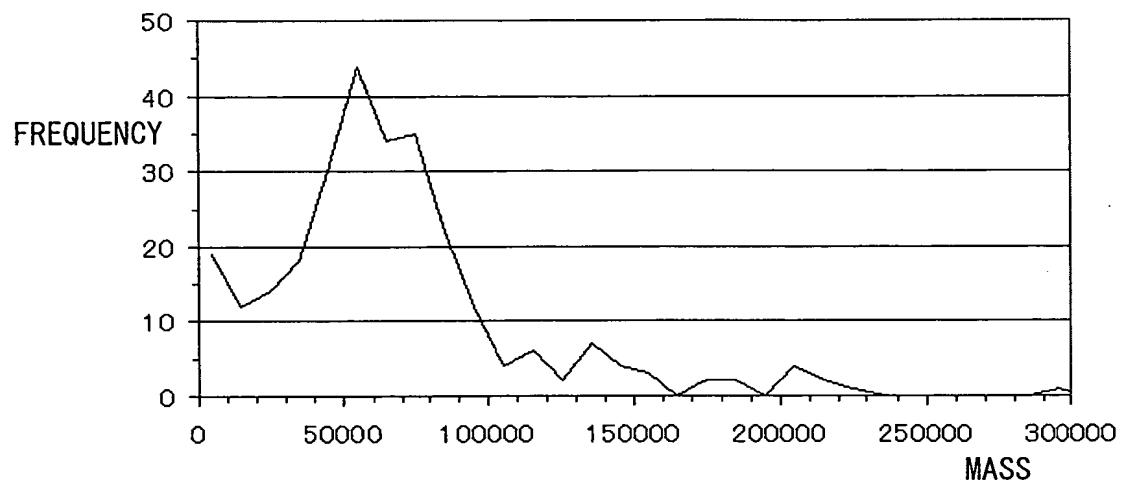


FIG. 8

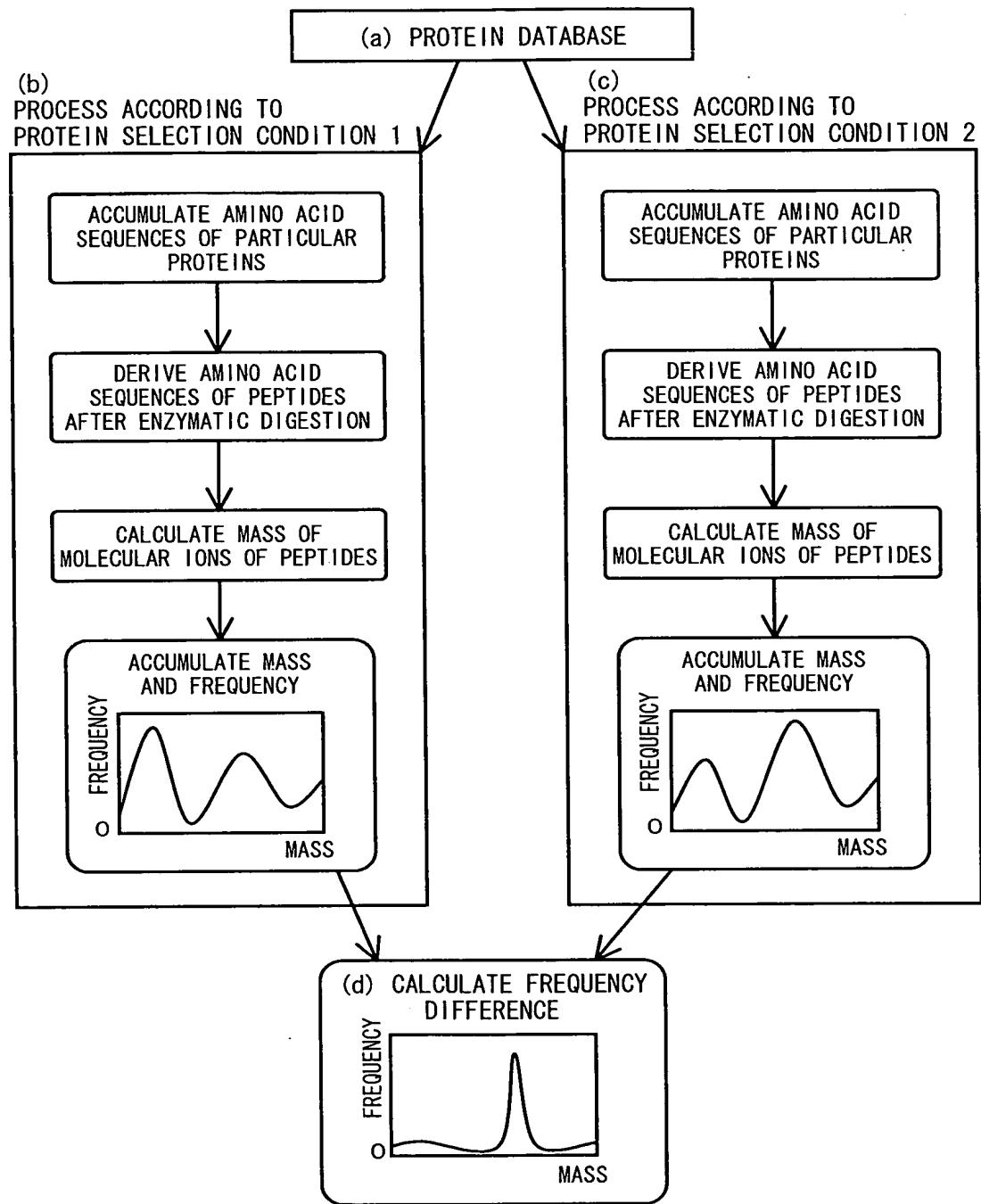


FIG. 9

